

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Olson, Eric N.
Grant, Stephen R.
Molkentin, Jeffrey D.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THERAPEUTIC
INTERVENTION IN CARDIAC HYPERTROPHY
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Arnold, White & Durkee
(B) STREET: P.O. Box 4433
(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE:
(C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McMillian, Nabeela R.
(B) REGISTRATION NUMBER: P-43,363
(C) REFERENCE/DOCKET NUMBER: UTSD:548
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTATCCTTTT GTTTTCCATC CTG

23

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCCTGCCTT TTCCAGCAAC GGT

23

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTCCAGGAT AAAAGGCCAC GGT

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACATTGGAA AATTTTATTA CAC

23

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGAAAAACAA

10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGGAAAAGGC

10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGATAAAG

10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Ala | Ser | Cys | Glu | Asp | Glu | Glu | Leu | Glu | Phe | Leu | Leu | Val |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Phe | Gly | Glu | Glu | Leu | Glu | Ala | Pro | Pro | Leu | Gly | Ala | Gly | Gly | Leu | Gly |
| | | | 20 | | | | 25 | | | | | 30 | | | |
| Glu | Glu | Leu | Asp | Ser | Glu | Asp | Ala | Pro | Pro | Cys | Cys | Arg | Leu | Ala | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Glu | Pro | Pro | Pro | Tyr | Gly | Ala | Ala | Pro | Ile | Gly | Ile | Pro | Arg | Pro |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Pro | Pro | Pro | Arg | Pro | Gly | Met | His | Ser | Pro | Pro | Pro | Arg | Pro | Ala | Pro |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ser | Pro | Gly | Thr | Trp | Glu | Ser | Gln | Pro | Ala | Arg | Ser | Val | Arg | Leu | Gly |
| | | | | 85 | | | | 90 | | | | | | 95 | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Gly | Pro | Gly | Gly | Gly | Ala | Gly | Gly | Ala | Gly | Gly | Gly | Arg | Val | Leu | Glu | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| Cys | Pro | Ser | Ile | Arg | Ile | Thr | Ser | Ile | Ser | Pro | Thr | Pro | Glu | Pro | Pro | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | |
| Ala | Ala | Leu | Glu | Asp | Asn | Pro | Asp | Ala | Trp | Gly | Asp | Gly | Ser | Pro | Arg | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | |
| Asp | Tyr | Pro | Pro | Pro | Glu | Gly | Phe | Gly | Gly | Tyr | Arg | Glu | Ala | Gly | Ala | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | |
| Gln | Gly | Gly | Gly | Ala | Phe | Phe | Ser | Pro | Ser | Pro | Gly | Ser | Ser | Ser | Leu | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | |
| Ser | Ser | Trp | Ser | Phe | Phe | Ser | Asp | Ala | Ser | Asp | Glu | Ala | Ala | Leu | Tyr | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | |
| Ala | Ala | Cys | Asp | Glu | Val | Glu | Ser | Glu | Leu | Asn | Glu | Ala | Ala | Ser | Arg | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | |
| Phe | Gly | Leu | Gly | Ser | Pro | Leu | Pro | Ser | Pro | Arg | Ala | Ser | Pro | Arg | Pro | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | |
| Trp | Thr | Pro | Glu | Asp | Pro | Trp | Ser | Leu | Tyr | Gly | Pro | Ser | Pro | Gly | Gly | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | |
| Arg | Gly | Pro | Glu | Asp | Ser | Trp | Leu | Leu | Leu | Ser | Ala | Pro | Gly | Pro | Thr | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | |
| Pro | Ala | Ser | Pro | Arg | Pro | Ala | Ser | Pro | Cys | Gly | Leu | Arg | Arg | Tyr | Ser | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | |
| Ser | Ser | Gly | Thr | Pro | Ser | Ser | Ala | Ser | Pro | Ala | Leu | Ser | Arg | Arg | Gly | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | |
| Ser | Leu | Gly | Glu | Glu | Gly | Ser | Glu | Pro | Pro | Pro | Pro | Pro | Pro | Leu | Pro | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | |
| Leu | Ala | Arg | Asp | Pro | Gly | Ser | Pro | Gly | Pro | Phe | Asp | Tyr | Val | Gly | Ala | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | |
| Pro | Pro | Ala | Glu | Ser | Ile | Pro | Gln | Leu | Thr | Arg | Arg | Thr | Ser | Ser | Glu | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | |
| Gln | Ala | Val | Ala | Leu | Pro | Arg | Ser | Glu | Glu | Pro | Ala | Ser | Cys | Asn | Gly | | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | | |
| Leu | Leu | Pro | Leu | Gly | Ala | Glu | Glu | Ser | Val | Ala | Pro | Pro | Gly | Gly | Ser | | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | | |
| Arg | Lys | Glu | Val | Ala | Gly | Met | Asp | Tyr | Leu | Ala | Val | Pro | Ser | Pro | Leu | | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Trp | Ser | Leu | Ala | Arg | Ile | Gly | Gly | His | Ser | Pro | Ile | Phe | Arg | Thr | 385 | 390 | 395 | 400 |
| Ser | Ala | Leu | Pro | Pro | Leu | Asp | Trp | Pro | Leu | Pro | Ser | Gln | Tyr | Glu | Gln | 405 | 410 | 415 | |
| Leu | Glu | Leu | Arg | Ile | Glu | Val | Gln | Pro | Arg | Ala | His | His | Arg | Ala | His | 420 | 425 | 430 | |
| Tyr | Glu | Thr | Glu | Gly | Ser | Arg | Gly | Ala | Val | Leu | Ala | Ala | Pro | Gly | Gly | 435 | 440 | 445 | |
| His | Pro | Val | Val | Leu | Leu | Leu | Gly | Tyr | Ser | Glu | Leu | Pro | Leu | Thr | Leu | 450 | 455 | 460 | |
| Gln | Met | Phe | Ile | Gly | Thr | Ala | Asp | Glu | Arg | Asn | Leu | Arg | Pro | His | Ala | 465 | 470 | 475 | 480 |
| Phe | Tyr | Gln | Val | His | Arg | Ile | Thr | Gly | Leu | Met | Val | Ala | Thr | Ala | Ser | 485 | 490 | 495 | |
| Tyr | Glu | Ala | Val | Val | Ser | Gly | Thr | Leu | Val | Leu | Glu | Met | Thr | Leu | Leu | 500 | 505 | 510 | |
| Pro | Glu | Asn | Asn | Met | Ala | Ala | Asn | Ile | Asp | Cys | Ala | Gly | Ile | Leu | Leu | 515 | 520 | 525 | |
| Leu | Arg | Asn | Ser | Asp | Ile | Glu | Leu | Arg | Lys | Gly | Glu | Thr | Asp | Ile | Gly | 530 | 535 | 540 | |
| Arg | Lys | Asn | Thr | Arg | Val | Arg | Leu | Val | Phe | Arg | Val | His | Val | Pro | Gln | 545 | 550 | 555 | 560 |
| Gly | Gly | Gly | Leu | Val | Val | Ser | Val | Gln | Ala | Ala | Ser | Val | Pro | Ile | Glu | 565 | 570 | 575 | |
| Cys | Ser | Gln | Arg | Ser | Ala | Gln | Glu | Leu | Pro | Gln | Val | Glu | Ala | Tyr | Ser | 580 | 585 | 590 | |
| Pro | Ser | Ala | Cys | Ser | Val | Arg | Gly | Gly | Glu | Glu | Leu | Val | Leu | Thr | Gly | 595 | 600 | 605 | |
| Ser | Asn | Phe | Leu | Pro | Asp | Ser | Leu | Val | Val | Phe | Ile | Glu | Arg | Gly | Pro | 610 | 615 | 620 | |
| Asp | Gly | Leu | Leu | Gln | Trp | Glu | Glu | Glu | Ala | Thr | Val | Asn | Arg | Leu | Gln | 625 | 630 | 635 | 640 |
| Ser | Asn | Glu | Val | Thr | Leu | Thr | Leu | Thr | Val | Pro | Glu | Tyr | Ser | Asn | Leu | 645 | 650 | 655 | |
| Arg | Val | Ser | Arg | Pro | Val | Gln | Val | Tyr | Phe | Tyr | Val | Ser | Asn | Gly | Arg | 660 | 665 | 670 | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Arg | Ser | Pro | Thr | Gln | Ser | Phe | Arg | Phe | Leu | Pro | Val | Ile | Cys |
| | | 675 | | | | | | 680 | | | | | 685 | | |
| Leu | Glu | Glu | Pro | Leu | Pro | Asp | Ser | Ser | Leu | Arg | Gly | Phe | Pro | Ser | Ala |
| | | 690 | | | | | 695 | | | | 700 | | | | |
| Ser | Ala | Thr | Pro | Phe | Gly | Thr | Asp | Met | Asp | Phe | Ser | Pro | Pro | Arg | Pro |
| | 705 | | | | | 710 | | | | 715 | | | | | 720 |
| Pro | Tyr | Pro | Ser | Tyr | Pro | His | Glu | Asp | Pro | Ala | Cys | Glu | Thr | Pro | Tyr |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Leu | Ser | Glu | Gly | Phe | Gly | Tyr | Gly | Met | Pro | Pro | Leu | Tyr | Pro | Gln | Thr |
| | | | 740 | | | | | 745 | | | | | | 750 | |
| Gly | Pro | Pro | Pro | Ser | Tyr | Arg | Pro | Gly | Leu | Arg | Met | Phe | Pro | Glu | Thr |
| | | | 755 | | | | | 760 | | | | 765 | | | |
| Arg | Gly | Thr | Thr | Gly | Cys | Ala | Gln | Pro | Pro | Ala | Val | Ser | Phe | Leu | Pro |
| | 770 | | | | | | 775 | | | | 780 | | | | |
| Arg | Pro | Phe | Pro | Ser | Asp | Pro | Tyr | Gly | Gly | Arg | Gly | Ser | Ser | Phe | Pro |
| | 785 | | | | | 790 | | | | 795 | | | | | 800 |
| Leu | Gly | Leu | Pro | Phe | Ser | Pro | Pro | Ala | Pro | Phe | Arg | Pro | Pro | Pro | Leu |
| | | | | 805 | | | | | 810 | | | | | 815 | |
| Pro | Ala | Ser | Pro | Pro | Leu | Glu | Gly | Pro | Phe | Pro | Ser | Gln | Ser | Asp | Val |
| | | | 820 | | | | | 825 | | | | | 830 | | |
| His | Pro | Leu | Pro | Ala | Glu | Gly | Tyr | Asn | Leu | Val | Gly | Pro | Gly | Tyr | Gly |
| | | 835 | | | | | 840 | | | | | 845 | | | |
| Pro | Gly | Glu | Gly | Ala | Pro | Glu | Gln | Glu | Leu | Ser | Arg | Gly | Gly | Tyr | Ser |
| | 850 | | | | | 855 | | | | | 860 | | | | |
| Ser | Gly | Phe | Arg | Asp | Ser | Val | Pro | Ile | Gln | Gly | Ile | Thr | Leu | Glu | Glu |
| | 865 | | | | | 870 | | | | 875 | | | | | 880 |
| Val | Ser | Glu | Ile | Ile | Gly | Arg | Asp | Leu | Ser | Gly | Phe | Pro | Ala | Pro | Pro |
| | | | | 885 | | | | | 890 | | | | | 895 | |
| Gly | Glu | Glu | Pro | Pro | Ala | | | | | | | | | | |
| | | | 900 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| GCTTCTGGAG | GGAGGCGGCA | GCGACGGAGG | AGGGGGCTTC | TCAGAGAAAG | GGAGGGAGGG | 60 |
| AGCCACCCGG | GTGAAGATAC | AGCAGCCTCC | TGAACTCCCC | CCTCCCACCC | AGGCCGGGAC | 120 |
| CTGGGGGCTC | CTGCCGGATC | CATGGGGGCG | GCCAGCTGCG | AGGATGAGGA | GCTGGAATTT | 180 |
| AAGCTGGTGT | TCGGGGAGGA | AAAGGAGGCC | CCCCCGCTGG | GCGCGGGGGG | ATTGGGGGAA | 240 |
| GAACTGGACT | CAGAGGATGC | CCCGCCATGC | TGCCGTCTGG | CCTTGGGAGA | GGCCCCCTCC | 300 |
| TATGGCGCTG | CACCTATCGG | TATTCCTCCG | CCTCCACCCC | CTCGGCCTGG | CATGCATTCT | 360 |
| CCACCGCCGC | GACCAGCCCC | CTCACCTGGC | ACCTGGGAGA | GCCAGCCCGC | CAGGTCGGTG | 420 |
| AGGCTGGGAG | GACCAGGAGG | GGGTGCTGGG | GGTGCTGGGG | GTGGCCGTGT | TCTCGAGTGT | 480 |
| CCCAGCATCC | GCATCACCTC | CATCTCTCCC | ACGCCGGAGC | CGCCAGCAGC | GCTGGAGGAC | 540 |
| AACCCTGATG | CCTGGGGGGA | CGGCTCTCCT | AGAGATTACC | CCCCACCAGA | AGGCTTTGGG | 600 |
| GGCTACAGAG | AAGCAGGGGC | CCAGGGTGGG | GGGGCCTTCT | TCAGCCCAAG | CCCTGGCAGC | 660 |
| AGCAGCCTGT | CCTCGTGGAG | CTTCTTCTCC | GATGCCTCTG | ACGAGGCAGC | CCTGTATGCA | 720 |
| GCCTGCGACG | AGGTGGAGTC | TGAGCTAAAT | GAGGCGGCCCT | CCCGCTTTGG | CCTGGGCTCC | 780 |
| CCGCTGCCCT | CGCCCCGGGC | CTCCCCCTCG | CCATGGACCC | CCGAAGATCC | CTGGAGCCTG | 840 |
| TATGGTCCAA | GGCCCGGAGG | CCGAGGGCCA | GAGGATAGCT | GGCTACTCCT | CAGTGCTCCT | 900 |
| GGGCCCACCC | CAGCCTCCCC | GCGGCCCTGC | TCTCCATGTG | GCAAGCGGCG | CTATTCCAGC | 960 |
| TCGGGAACCC | CATCTTCAGC | CTCCCCAGCT | CTGTCCCGCC | GTGGCAGCCT | GGGGGAAGAG | 1020 |
| GGGTCTGAGC | CACCTCCACC | ACCCCCATTG | CCTCTGGCCC | GGGACCCGGG | CTCCCCCTGGT | 1080 |
| CCCTTTGACT | ATGTGGGGGC | CCCACCAGCT | GAGAGCATCC | CTCAGAAGAC | ACGGCGGACT | 1140 |
| TCCAGCGAGC | AGGCAGTGGC | TCTGCCCTCG | TCTGAGGAGC | CTGCCTCATG | CAATGGGAAG | 1200 |
| CTGCCCTTGG | GAGCAGAGGA | GTCTGTGGCT | CCTCCAGGAG | GTTCCTCGAA | GGAGGTGGCT | 1260 |
| GGCATGGACT | ACCTGGCAGT | GCCCTCCCCA | CTCGCTTGGT | CCAAGGCCCG | GATTGGGGGA | 1320 |
| CACAGCCCTA | TCTTCAGGAC | CTCTGCCCTA | CCCCACTGG | ACTGGCCTCT | GCCCAGCCAA | 1380 |
| TATGAGCAGC | TGGAGCTGAG | GATCGAGGTA | CAGCCTAGAG | CCCACCACCG | GGCCCACTAT | 1440 |
| GAGACAGAAG | GCAGCCGTGG | AGCTGTCAAA | GCTGCCCTTG | GCGGTCACCC | CGTAGTCAAG | 1500 |
| CTCCTAGGCT | ACAGTGAGAA | GCCACTGACC | CTACAGATGT | TCATCGGCAC | TGCAGATGAA | 1560 |

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|------|
| AGGAACCTGC | GGCCTCATGC | CTTCTATCAG | GTGCACCGTA | TCACAGGCAA | GATGGTGGCC | 1620 |
| ACGGCCAGCT | ATGAAGCCGT | AGTCAGTGGC | ACCAAGGTGT | TGGAGATGAC | TCTGCTGCCT | 1680 |
| GAGAACAACA | TGGCGGCCAA | CATTGACTGC | GCGGGAATCC | TGAAGCTTCG | GAATTCAGAC | 1740 |
| ATTGAGCTTC | GGAAGGGTGA | GACGGACATC | GGGCGCAAAA | ACACACGTGT | ACGGCTGGTG | 1800 |
| TTCCGGGTAC | ACGTGCCCCA | GGGCGGCGGG | AAGGTCGTCT | CAGTACAGGC | AGCATCGGTG | 1860 |
| CCCATCGAGT | GCTCCCAGCG | CTCAGCCCAG | GAGCTGCCCC | AGGTGGAGGC | CTACAGCCCC | 1920 |
| AGTGCCCTGCT | CTGTGAGAGG | AGGCGAGGAA | CTGGTACTGA | CCGGCTCCAA | CTTCCTGCCA | 1980 |
| GACTCCAAGG | TGGTGTTCAT | TGAGAGGGGT | CCTGATGGGA | AGCTGCAATG | GGAGGAGGAG | 2040 |
| GCCACAGTGA | ACCGACTGCA | GAGCAACGAG | GTGACGCTGA | CCCTGACTGT | CCCCGAGTAC | 2100 |
| AGCAACAAGA | GGGTTTCCCG | GCCAGTCCAG | GTCTACTTTT | ATGTCTCCAA | TGGGCGGAGG | 2160 |
| AAACGCAGTC | CTACCCAGAG | TTTCAGGTTT | CTGCCTGTGA | TCTGCAAAGA | GGAGCCCCTA | 2220 |
| CCGGACTCAT | CTCTGCGGGG | TTTCCCTTCA | GCATCGGCAA | CCCCCTTTGG | CACTGACATG | 2280 |
| GACTTCTCAC | CACCCAGGCC | CCCCTACCCC | TCCTATCCCC | ATGAAGACCC | TGCTTGCGAA | 2340 |
| ACTCCTTACC | TATCAGAAGG | CTTCGGCTAT | GGCATGCCCC | CTCTGTACCC | CCAGACGGGG | 2400 |
| CCCCCACCAT | CCTACAGACC | GGGCCTGCGG | ATGTTCCCTG | AGACTAGGGG | TACCACAGGT | 2460 |
| TGTGCCCAAC | CACCTGCAGT | TTCCTTCCTT | CCCCGCCCCCT | TCCCTAGTGA | CCCGTATGGA | 2520 |
| GGGCGGGGCT | CCTCTTTCCC | CCTGGGGCTG | CCATTCTCTC | CGCCAGCCCC | CTTTCGGCCG | 2580 |
| CCTCCTCTTC | CTGCATCCCC | ACCGCTTGAA | GGCCCCTTCC | CTTCCCAGAG | TGATGTGCAT | 2640 |
| CCCCTACCTG | CTGAGGGATA | CAATAAGGTA | GGGCCAGGCT | ATGGCCCTGG | GGAGGGGGCT | 2700 |
| CCGGAGCAGG | AGAAATCCAG | GGGTGGCTAC | AGCAGCGGCT | TTCGAGACAG | TGTCCCTATC | 2760 |
| CAGGGTATCA | CGCTGGAGGA | AGTGAGTGAG | ATCATTTGGCC | GAGACCTGAG | TGGCTTCCCT | 2820 |
| GCACCTCCTG | GAGAAGAGCC | TCCTGCCTGA | ACCACGTGAA | CTGTCATCAC | CTGGCAACCC | 2880 |
| C | | | | | | 2881 |